

Figure 1A.

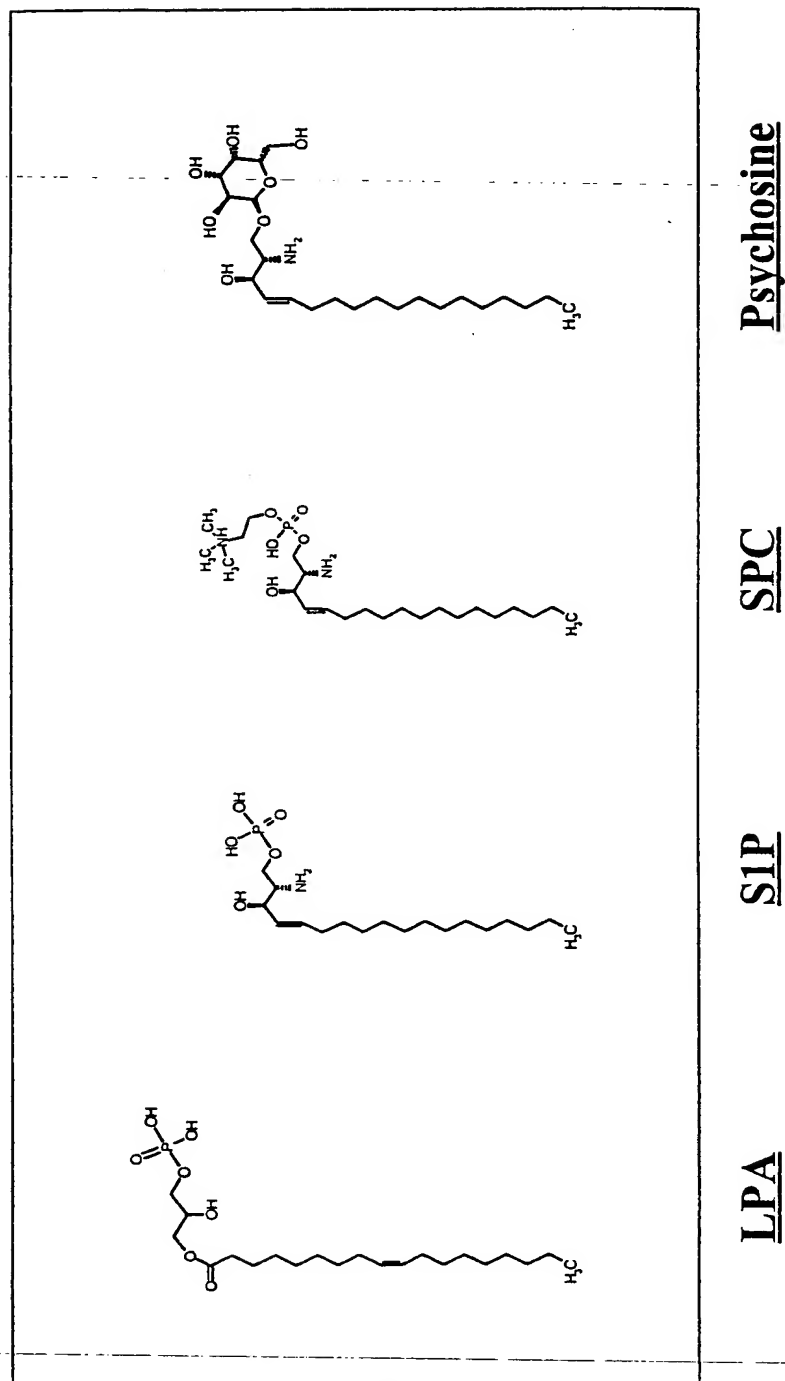


Figure 1B.

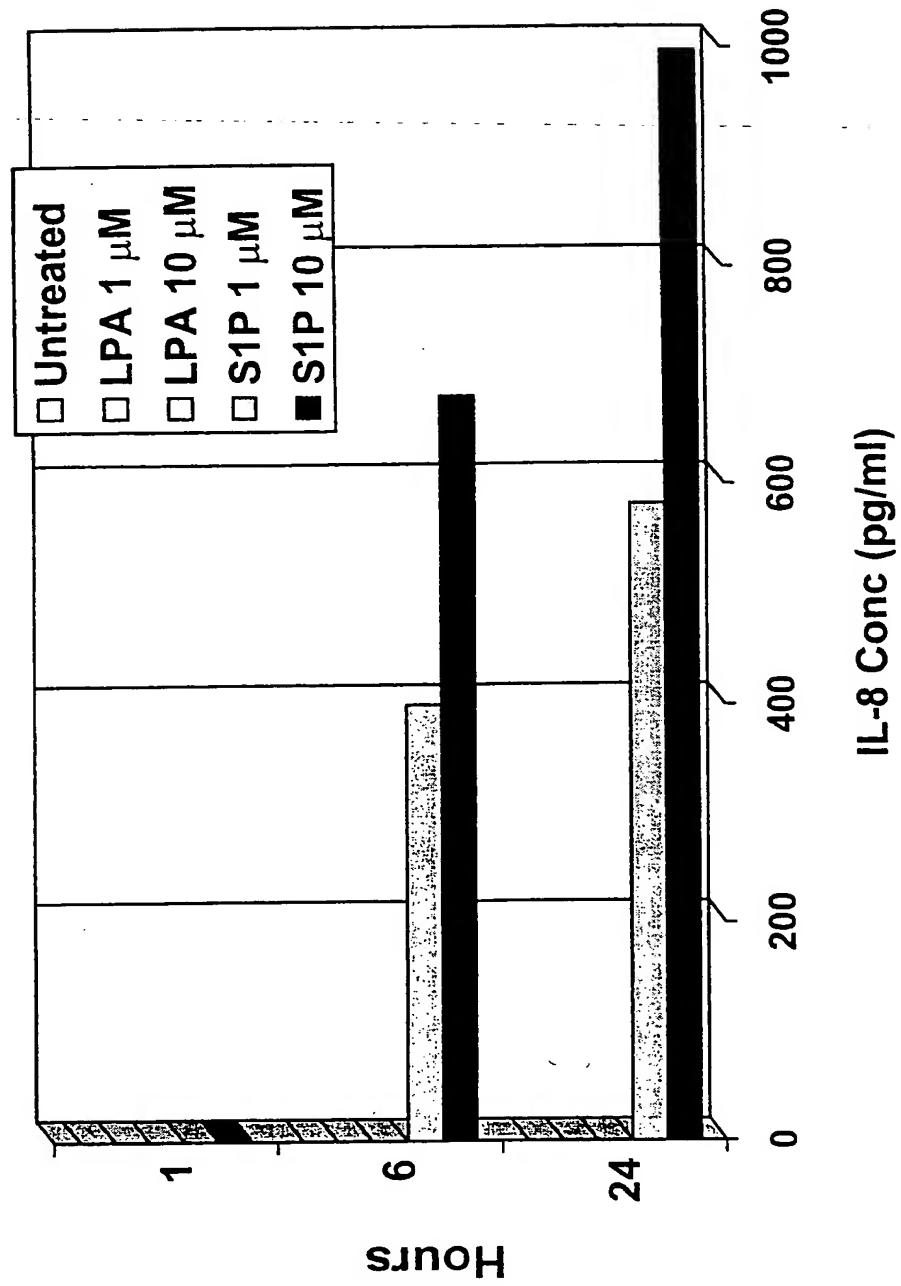


Figure 2A.

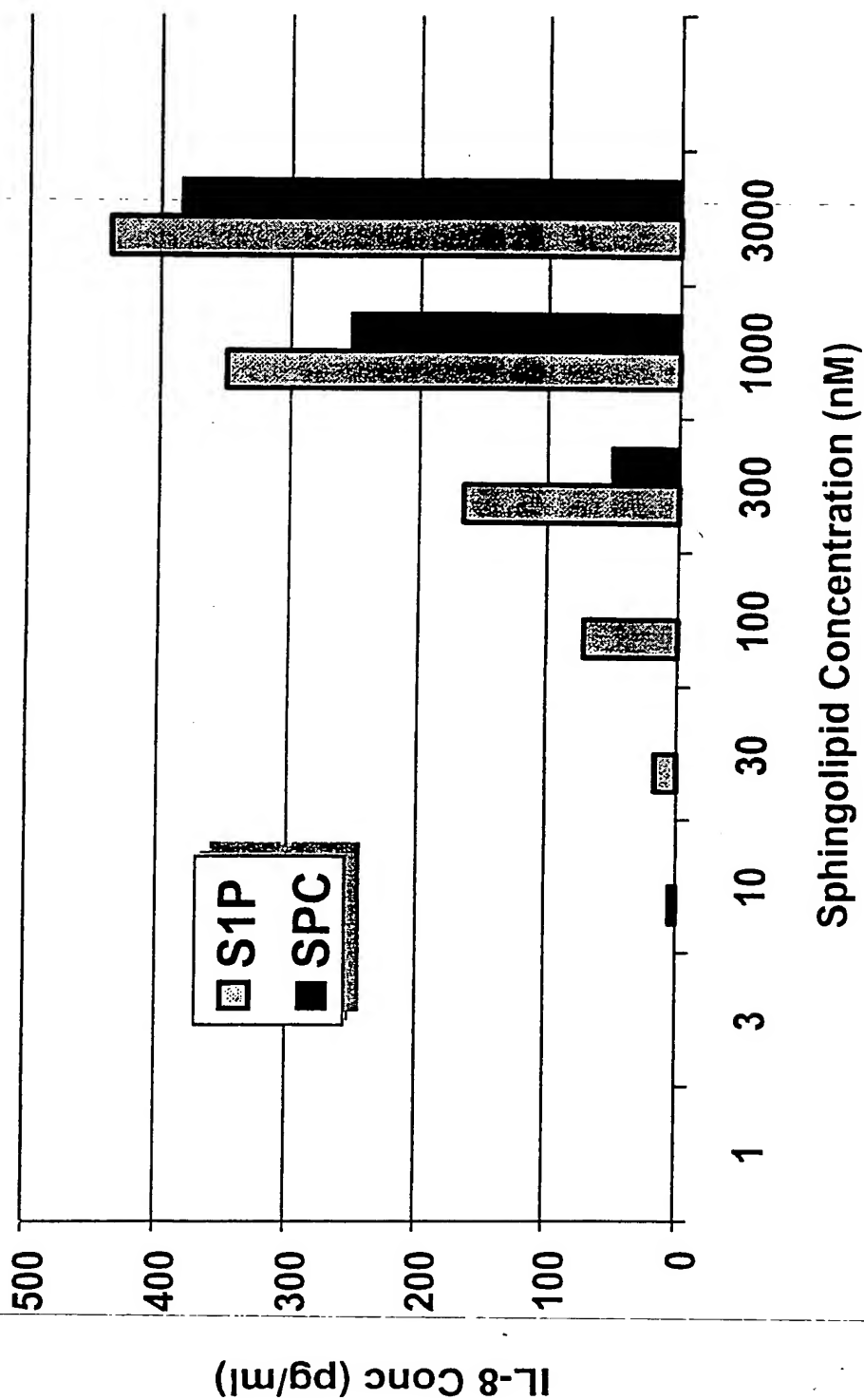


FIGURE 2

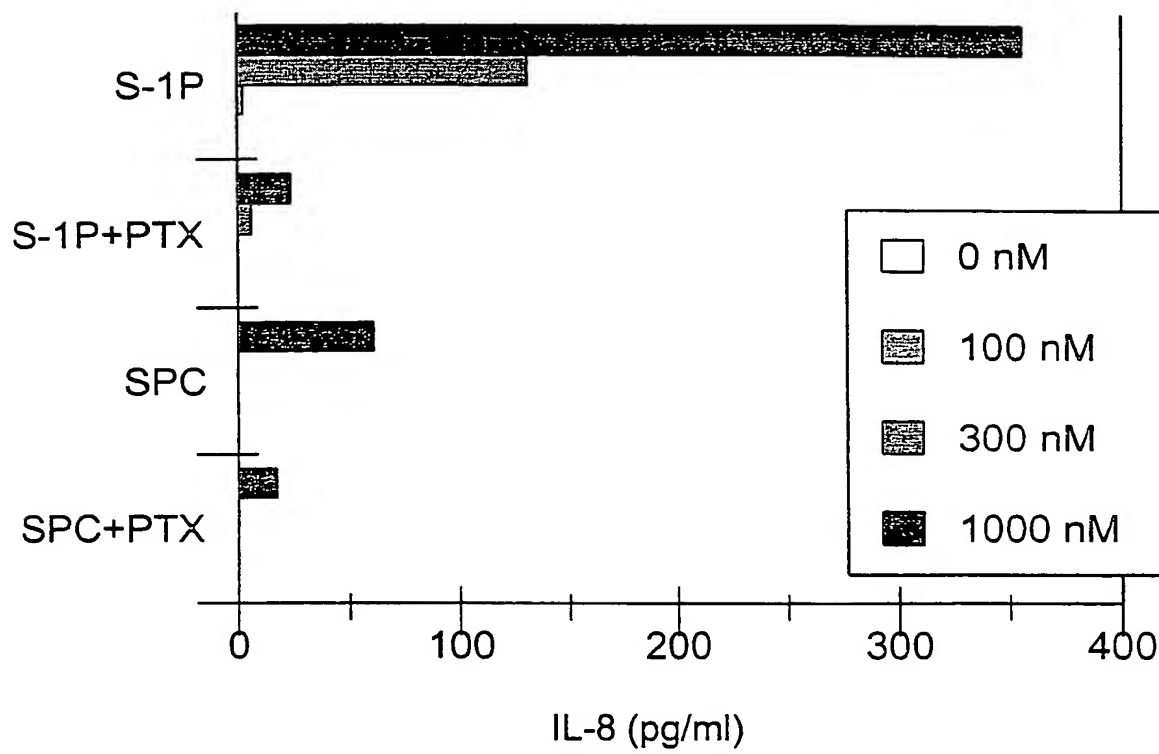


Figure 3.

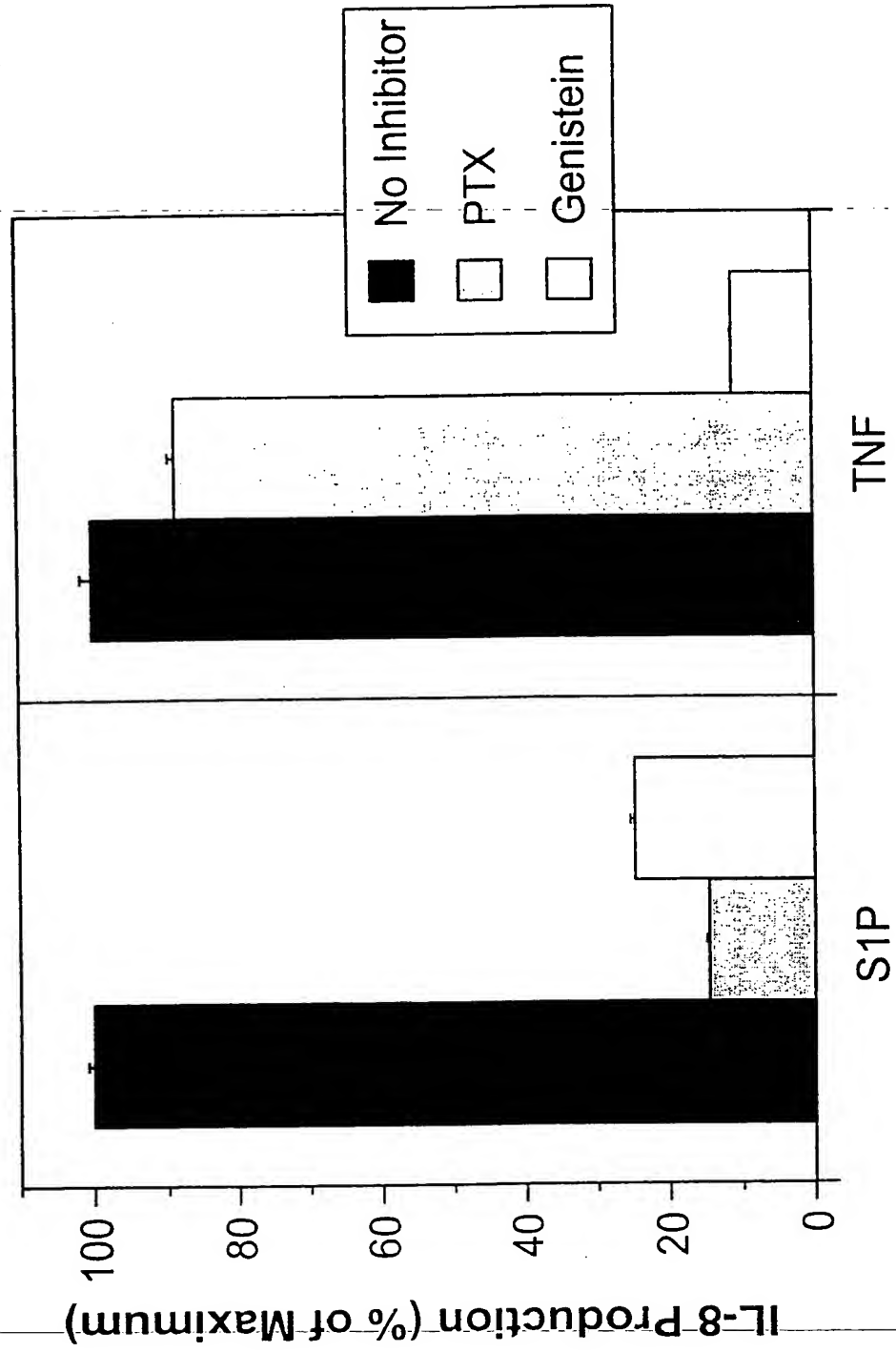


FIGURE 4A

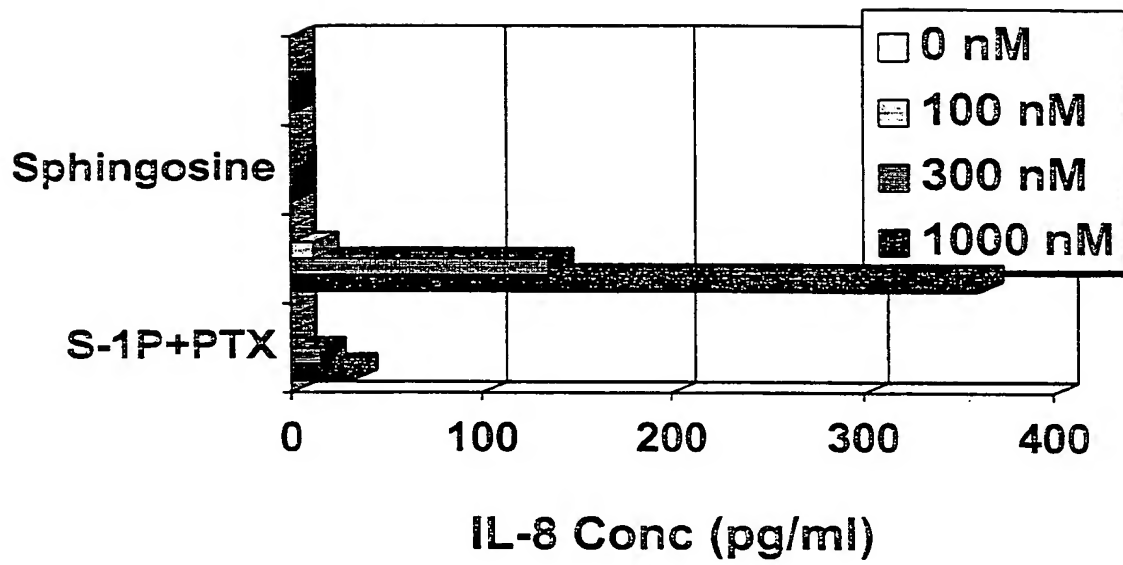


Figure 4B.

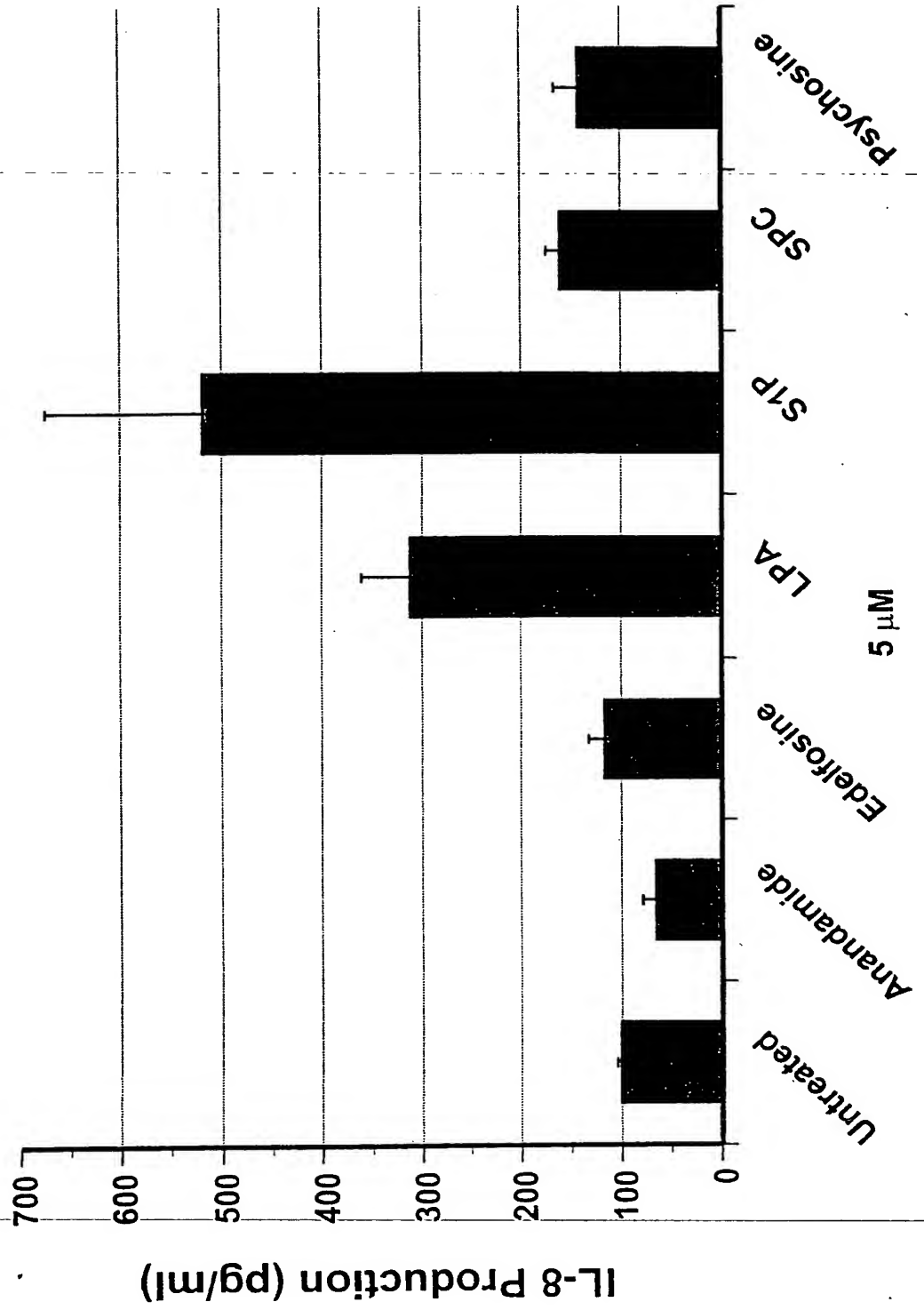


Figure 5.

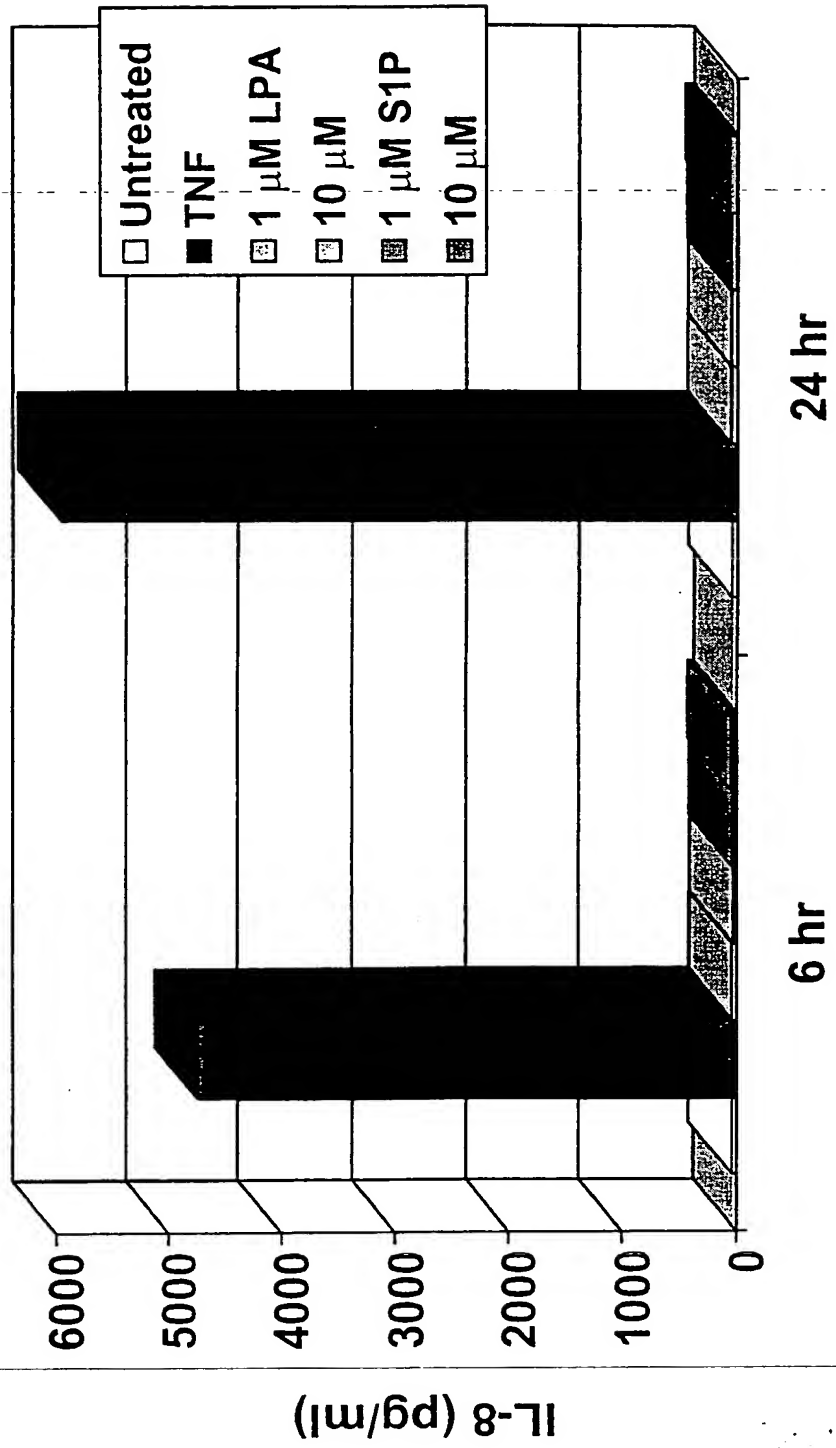
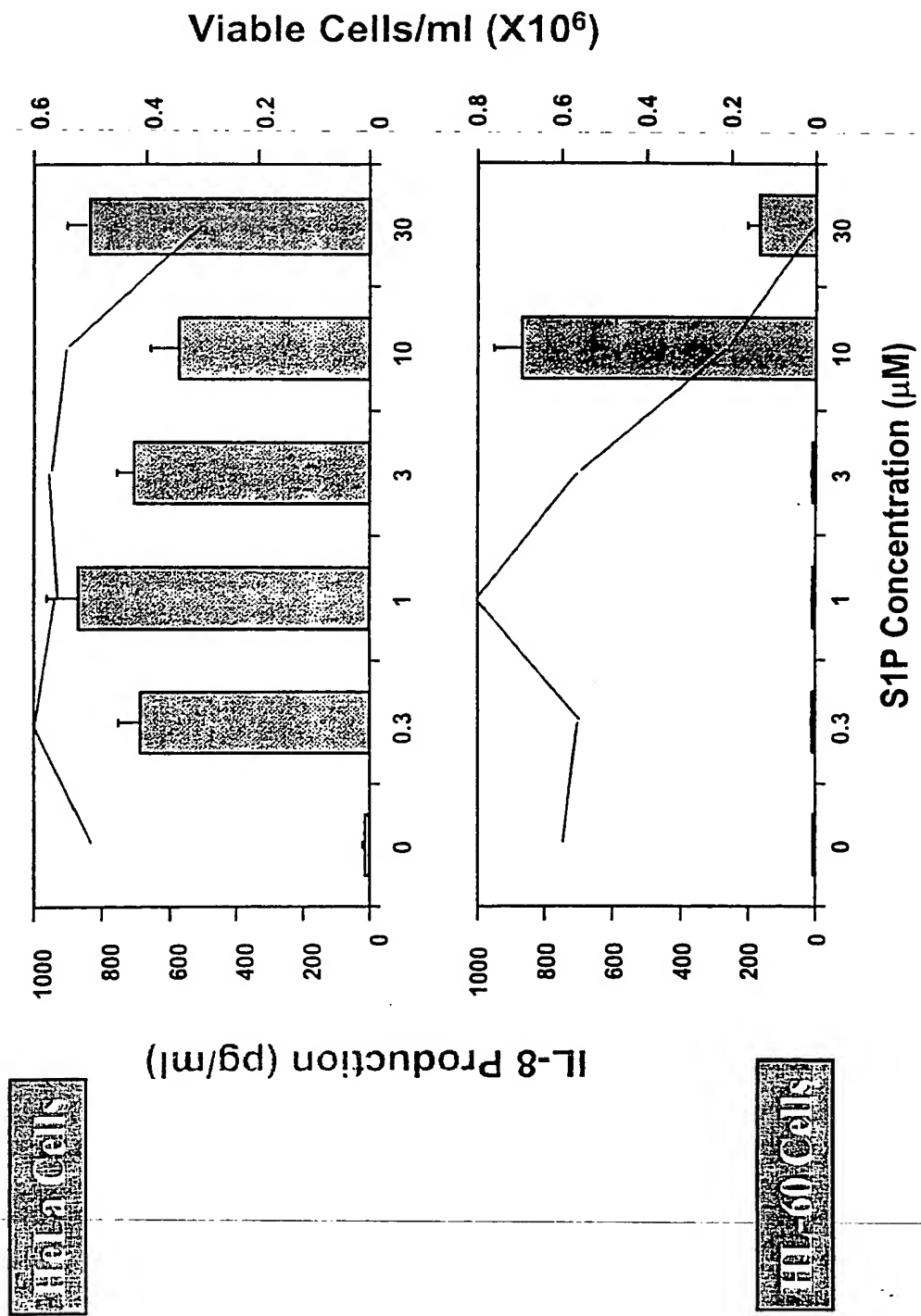


Figure 6.



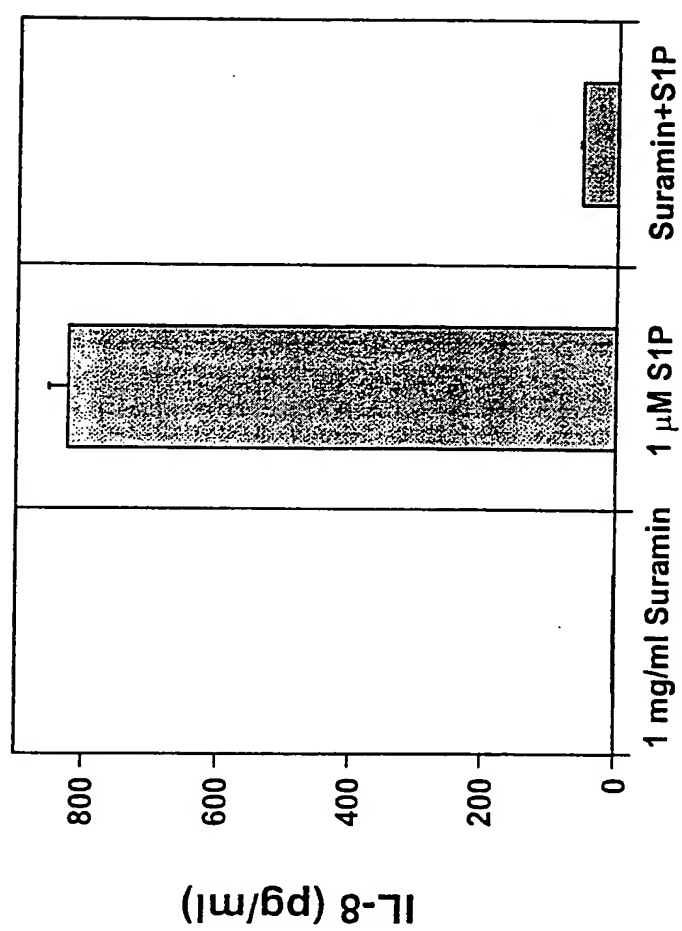


Figure 7.

Figure 8.

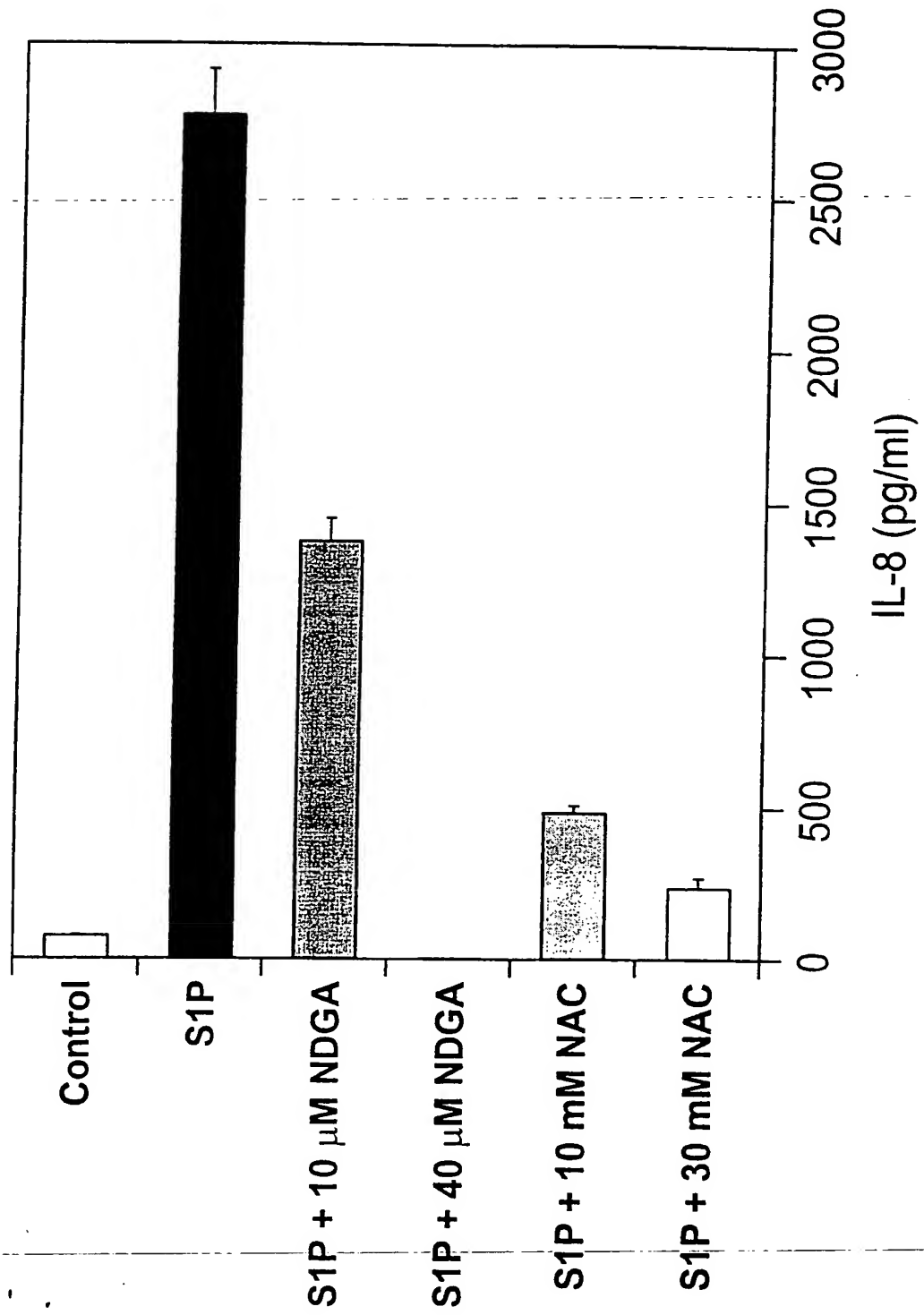


Figure 9.

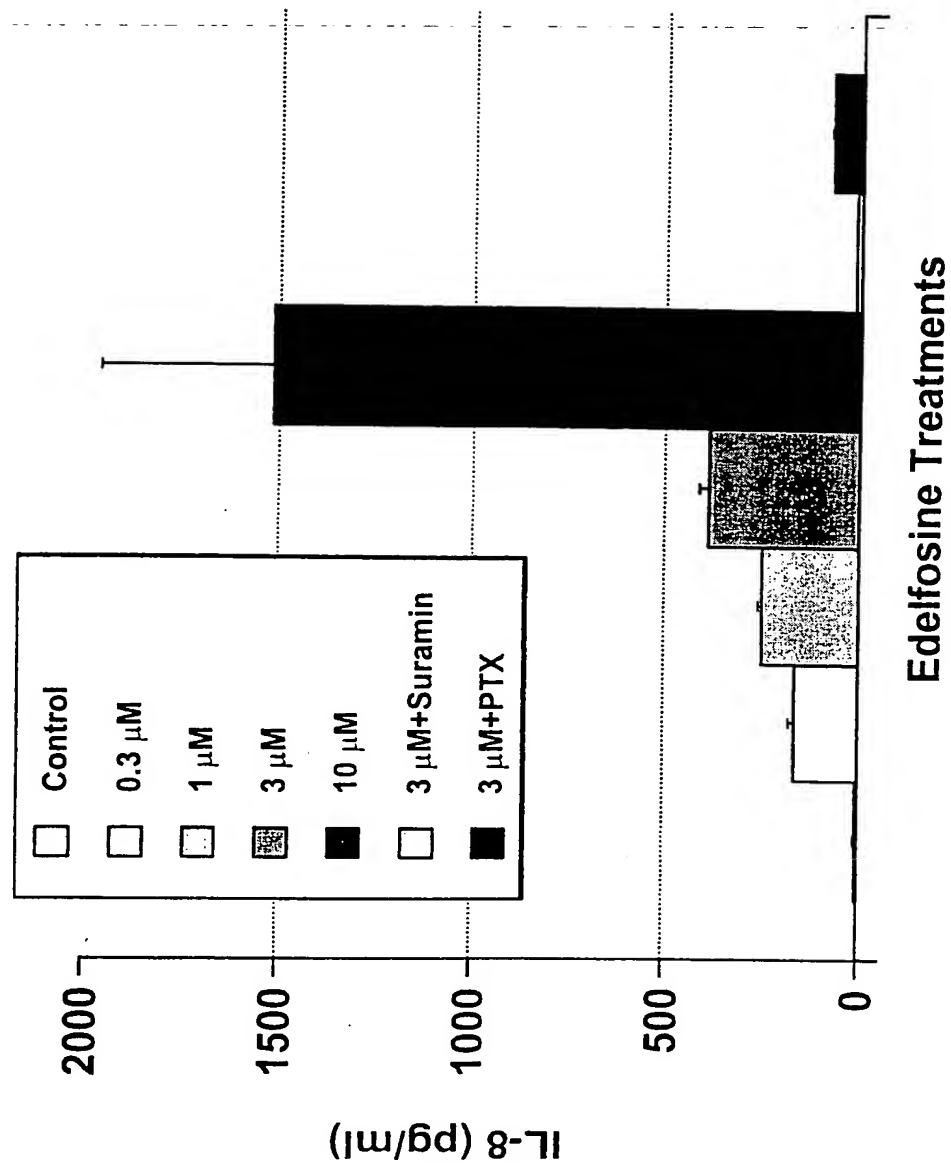


FIGURE 10A

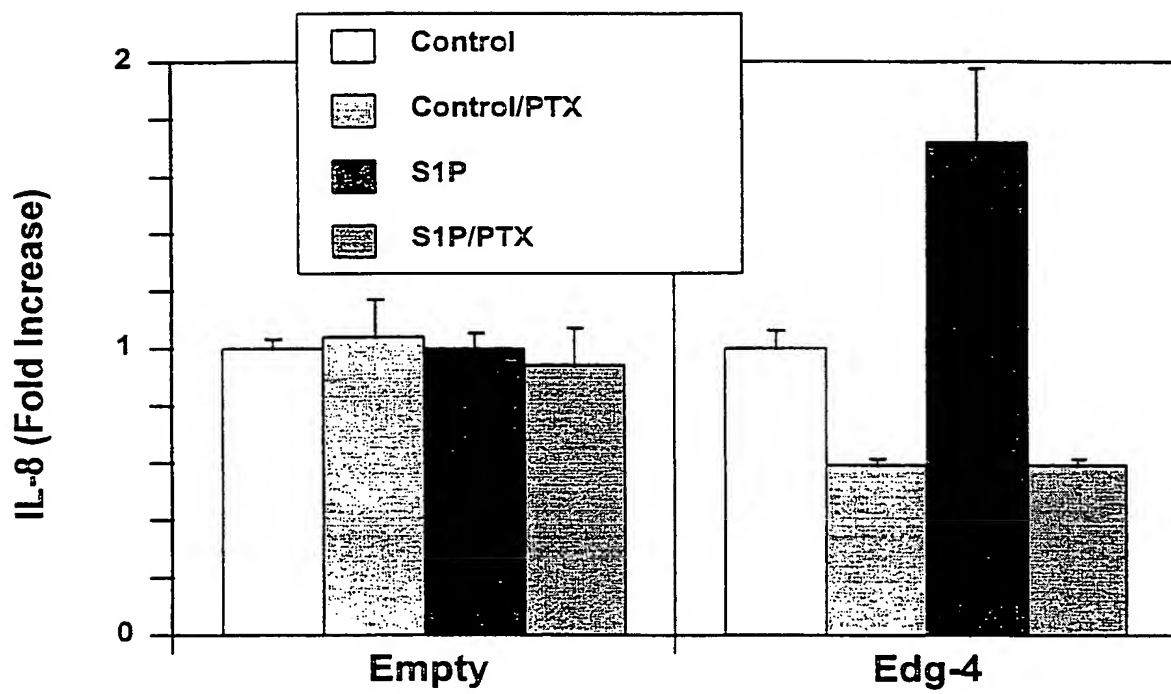


Figure 10B

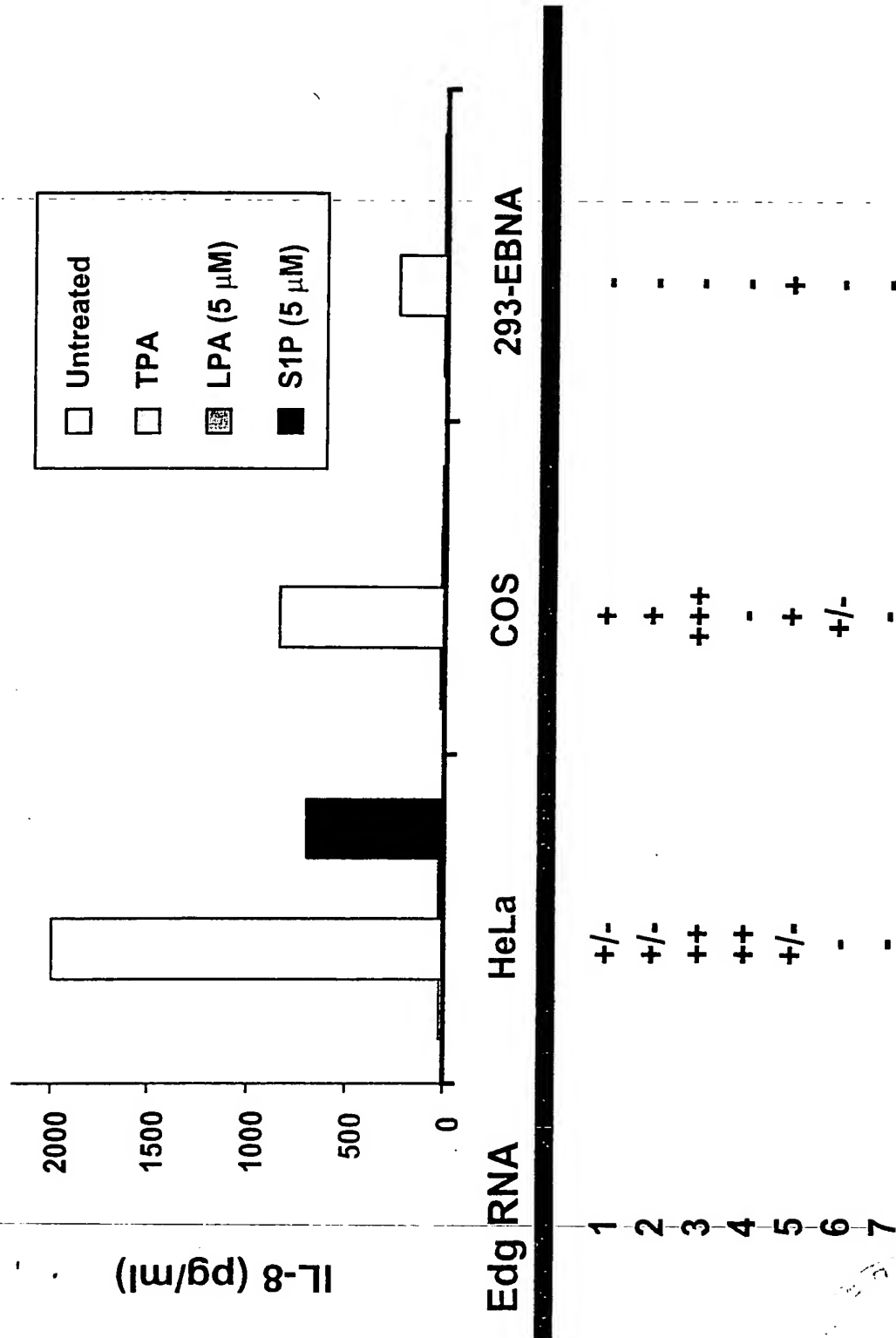


Figure 11.

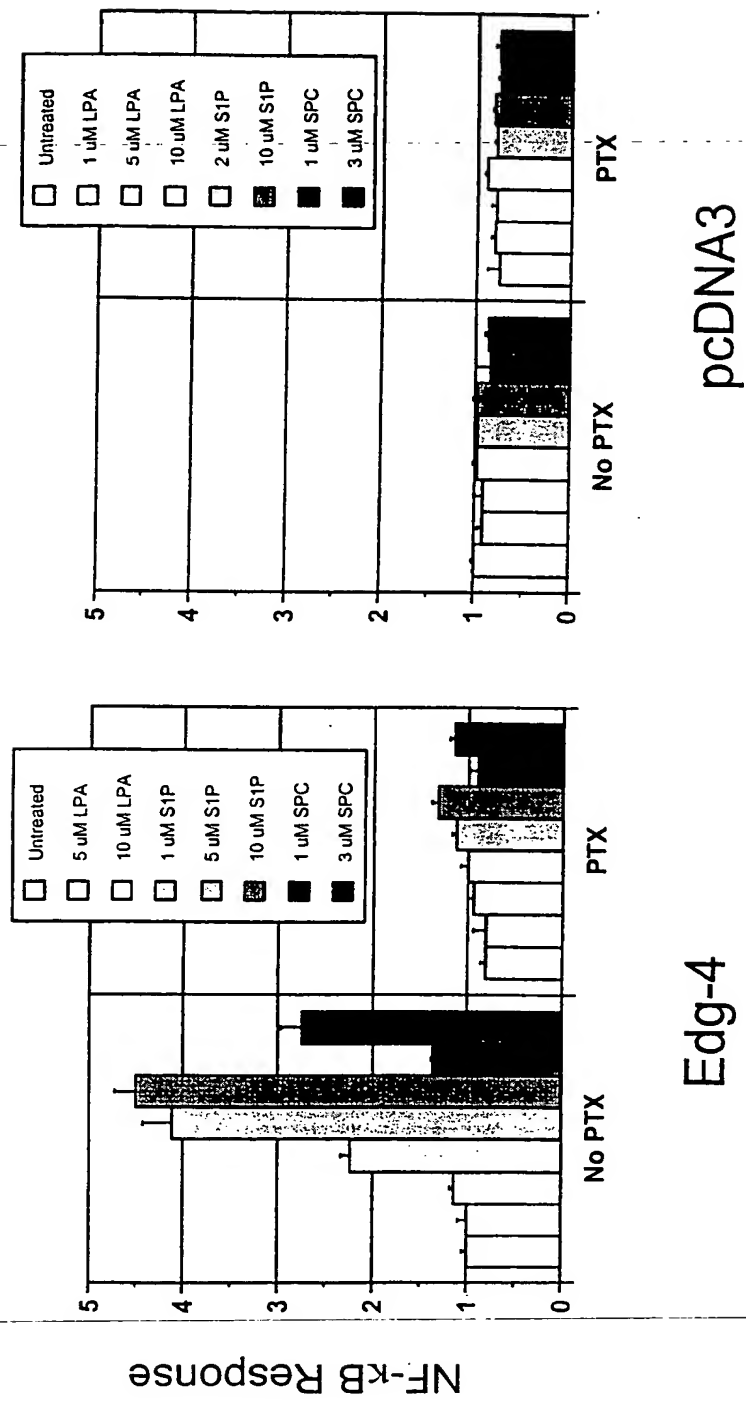


Figure 12.

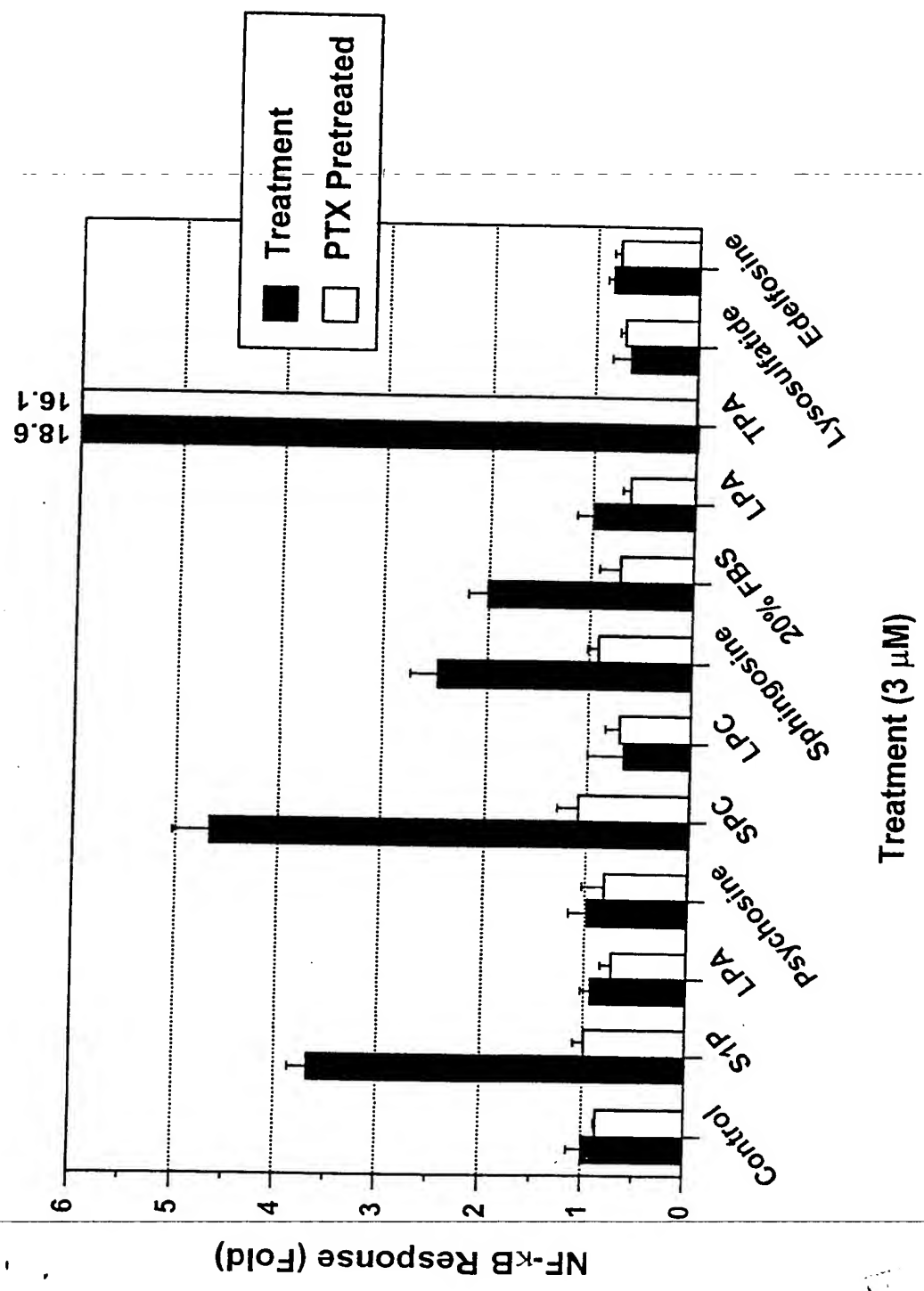


Figure 13.

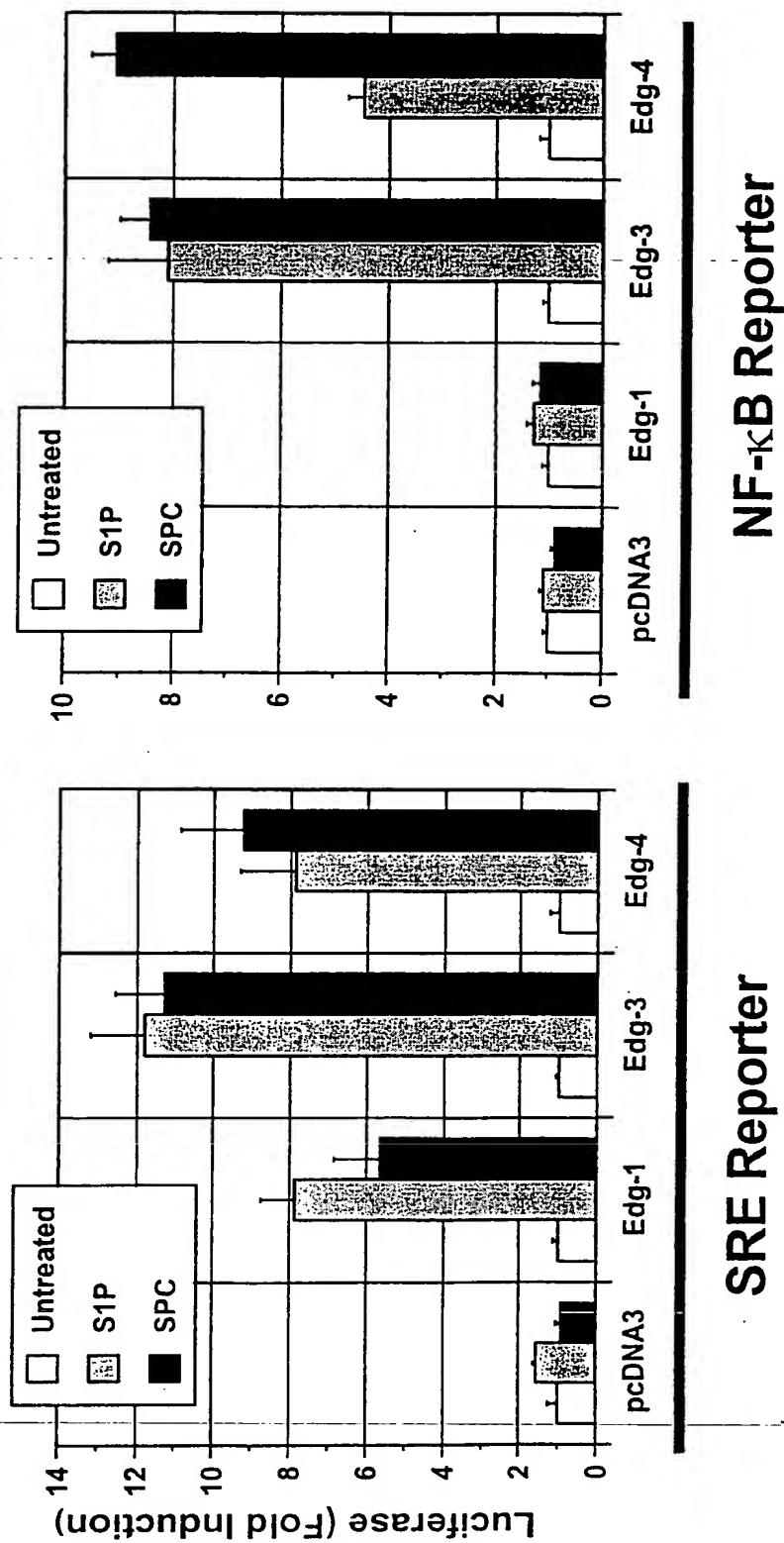


FIGURE 14

1					50
AA834537	-----AAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC	CACCATGGGC
AA804628	-----AAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC	CACCATGGGC
AA827835	AGTTCTGAAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC	CACCATGGGC
	51				100
AA834537	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG	AACACTATAA
AA804628	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG	AACACTATAA
AA827835	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG	AACACTATAA
	101				150
AA834537	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC	CGCCAGGTGG
AA804628	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC	CGCCAGGTGG
AA827835	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC	CGCCAGGTGG
	151				200
AA834537	CCTCGGCATT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT	GGAAAACCTT
AA804628	CCTCGGCCTT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT	GGAAAACCTT
AA827835	GCTCGGCCTT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT	GGAAAACCTT
	201				250
AA834537	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT	CGGCAATGTA
AA804628	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT	CGGCAATGTA
AA827835	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT	CGGCAATGTA
	251				300
AA834537	CCTGTTTCTG	GGCAACCTGG	CCGCCTCCGA	TCTACTGGCA	GGCGTGGCCT
AA804628	CCTGTTTCTG	GGCAACCTGG	CCGCCTCCGA	TCTACTGGCA	GGCGTGGCCT
AA827835	CCTGTTTCTG	GGCAACCTGG	CCGCCTCCGA	TCTACTGGCA	GGCGTGG . CT
	301				350
AA834537	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG	GCTGACGCCT
AA804628	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG	GCTGACGCCT
AA827835	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG	GCTGACGCCT
	351				400
AA834537	GTGCAGTGGT	TTGCCC GGGA	CGGTCTGCCT	TCATCACGCT	CTCGGCCTCT
AA804628	GTGCAGTGGT	TTGCCC GGGA	C-----	-----	-----
AA827835	GTGCAGTGGT	TTGCCC GGGA	-----	-----	-----
	401				450
AA834537	GTCTTCAGCC	TCCTGGCCAT	CGCCATTGAG	CGCCACGTGG	CCATTGCAAA
AA804628	-----	-----	-----	-----	-----
AA827835	-----	-----	-----	-----	-----
	451				
AA834537	GG				
AA804628	--				
AA827835	--				

FIGURE 15 A

M G S L Y S E Y
1 AAAGCCCCATGGCCCCAGCAGGCCTCTGAGCCCCACCATGGGCAGCTTGTACTCGGAGTA 60
-----+-----+-----+-----+-----+-----+
TTTCGGGGTACCGGGGTCGTCCGGAGACTCGGGGTGGTACCCGTGCAACATGAGCCTCAT
L N P N K V Q E H Y N Y T K E T L E T Q
61 CCTGAACCCCAACAAGGTCCAGGAACACTATAATTATACCAAGGAGACGCTGGAAACGCA 120
-----+-----+-----+-----+-----+-----+
GGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATATGGTTCTCTGCGACCTTTGCGT
E T T S R Q V A S A F I V I L C C A I V
121 GGAGACGACCTCCCGCCAGGTGGCCTCGGCCTTCATCGTCATCCTCTGTTGCGCCATTGT 180
-----+-----+-----+-----+-----+-----+
CCTCTGCTGGAGGGCGGTCCACCGAGCCGGAAGTAGCAGTAGGAGACAACCGGGTAACA
V E N L L V L I A V A R N S K F H S A M
181 GGTGGAACCTTCTGGTGCTCATTGCGGTGGCCCCGAAACAGCAAGTTCCTCGGCAAT 240
-----+-----+-----+-----+-----+-----+
CCACCTTTTGAAGACCACGAGTAACGCCACCGGGCTTTGTCGTTCAAGGTGAGCCGTTA
Y L F L G N L A A S D L L A G V A F V A
241 GTACCTGTTTCTGGGCAACCTGGCCGCTCCGATCTACTGGCAGGCGTGGCCTTCGTAGC 300
-----+-----+-----+-----+-----+-----+
CATGGACAAAGACCCGTTGGACCGGCGGAGGCTAGATGACCGTCCGCACCGGAAGCATCG
N T L L S G S V T L R L T P V Q W F A R
301 CAATACCTTGCTCTCTGGCTCTGTACGCTGAGGCTGACGCTGTGCAGTGGTTTGCCCG 360
-----+-----+-----+-----+-----+-----+
GTTATGGAACGAGAGACCGAGACAGTGCGACTCCGACTGCGGACACGTACCAACCGGGC
E G S A F I T L S A S V F S L L A I A I
361 GGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTCTTCAGCCTCCTGGCCATCGCCAT 420
-----+-----+-----+-----+-----+-----+
CCTCCCGAGACGGAAGTAGTGCGAGAGCCGAGACAGAAGTCGGAGGACCGGTAGCGGTA
E R H V A I A K V K L Y G S D K S C R M
421 TGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTATGGCAGCGACAAGAGCTGCCGCAT 480
-----+-----+-----+-----+-----+-----+
ACTCGCGGTGCACCGGTAACGGTTCAGTTTCGACATACCGTCTGCTGTTCTCGACGGCGTA
L L L I G A S W L I S L V L G G L P I L
481 GCTTCTGCTCATCGGGGCTCGTGGCTCATCTCGCTGGTCCCTCGGTGGCCTGCCCATCCT 540
-----+-----+-----+-----+-----+-----+
CGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGACAGGAGCCACCGGACGGGTAGGA
G W N C L G H L E A C S T V L P L Y A K
541 TGGCTGGAACCTGCCTGGGCCACCTCGAGGCTGCTCCACTGTCTGCTCTCTACGCCAA 600
-----+-----+-----+-----+-----+-----+
ACCGACCTTGACGGACCCGGTGGAGCTCCGACGAGGTGACAGGACGAGAGATGCGGTT
H Y V L C V V T I F S I I L L A I V A L
601 GCATTATGTGCTGTGCTGGTGACCATCTTCCATCATCCTGTTGGCCATCGTGGCCCT 660
-----+-----+-----+-----+-----+-----+
CGTAATACACGACACGCACCACTGGTAGAAGAGGTAGTAGGACAACCGGTAGCACCGGGA

Figure 15B**cDNA sequence of clone pC3-hedg4#36 encoding functional HEDG4 receptor protein.**

```

1  ATGGGCAGCTTGTACTCGGAGTACCTGAACCCCAACAAGGTCCAGGAACACTATAATTAT  60
   -----+-----+-----+-----+-----+-----+
   TACCCGTCGAACATGAGCCTCATGGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATA
61  ACCAAGGAGACGCTGGAAACGCAGGAGACGACCTCCCGCCAGGTGGCCTCGGCCTTCATC  120
   -----+-----+-----+-----+-----+-----+
   TGGTTCCTCTGCGACCTTTGCGTCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAG
121  GTCATCCTCTGTTGCGCCATTGTGGTGGAAAACCTTCTGGTGCTCATTGCGGTGGCCCGA  180
   -----+-----+-----+-----+-----+-----+
   CAGTAGGAGACAACGCGGTAACACCACCTTTTGAAGACCACGAGTAACGCCACCGGGCT
181  AACAGCAAGTTCCACTCGGCAATGTACCTGTTTCTGGGCAACCTGGCCGCCTCCGATCTA  240
   -----+-----+-----+-----+-----+-----+
   TTGTCGTTCAAGGTGAGCCGTTACATGGACAAAGACCCGTTGACCGGCGGAGGCTAGAT
241  CTGGCAGGCGTGGCCTTCGTAGCCAATACCTTGCTCTCTGGCTCTGTCACGCTGAGGCTG  300
   -----+-----+-----+-----+-----+-----+
   GACCGTCCGCACCGGAAGCATCGGTTATGGAACGAGAGACCGGAGACAGTGCGACTCCGAC
301  ACGCCTGTGCAGTGGTTTGCCCGGGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTC  360
   -----+-----+-----+-----+-----+-----+
   TGCGGACACGTCACCAAACGGGCCCTCCCGAGACGGAAGTAGTGCGAGAGCCGGAGACAG
361  TTCAGCCTCTGGCCATCGCCATTGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTAT  420
   -----+-----+-----+-----+-----+-----+
   AAGTCGGAGGACCGGTAGCGGTAACCTCGCGGTGCACCGGTAACGGTTCCAGTTCGACATA
421  GGCAGCGACAAGAGCTGCCGCATGCTTCTGCTCATCGGGGCCTCGTGGCTCATCTCGCTG  480
   -----+-----+-----+-----+-----+-----+
   CCGTCGCTGTTCTCGACGGCGTACGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGAC
481  GTCCTCGGTGGCCTGCCCATCCTTGGCTGGAAGTGCCTGGGCCACCTCGAGGCCTGCTCC  540
   -----+-----+-----+-----+-----+-----+
   CAGGAGCCACCGGACGGGTAGGAACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGG
541  ACTGTCCTGCCTCTCTACGCCAAGCATTATGTGCTGTGCGTGGTGACCATCTTCTCCATC  600
   -----+-----+-----+-----+-----+-----+
   TGACAGGACGGAGAGATGCGGTTGTAATACACGACACGCACCACTGGTAGAAGAGGTAG
601  ATCCTGTTGGCCGTCGTGGCCCTGTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCAC  660
   -----+-----+-----+-----+-----+-----+
   TAGGACAACCGGCAGCACCGGGACATGCACGCGTAGATGACGCACCAGGCGAGTTCGGTG
661  GCTGACATGGCCGCCCGCGAGACGCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGC  720
   -----+-----+-----+-----+-----+-----+
   CGACTGTACCGGCGGGGCGTCTGCGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCG
721  GTCTTTATCGTCTGCTGGCTGCCCGCCTTCAGCATCCTCCTTCTGGACTATGCCTGTCCC  780
   -----+-----+-----+-----+-----+-----+

```

CAGAAATAGCAGACGACCGACGGGCGGAAGTCGTAGGAGGAAGACCTGATACGGACAGGG
781 GTCCACTCCTGCCCGATCCTCTACAAAGCCCACTACCTTTTCGCCGTCTCCACCCTGAAT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CAGGTGAGGACGGGCTAGGAGATGTTTCGGGTGATGGAAAAGCGGCAGAGGTGGGACTTA 840
TCCCTGCTCAACCCCGTCATCTACACGTGGCGCAGCCGGGACCTGCGGCGGGAGGTGCTT
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
AGGGACGAGTTGGGGCAGTAGATGTGCACCGCGTCGGCCCTGGACGCCGCCCTCCACGAA 900
CGGCCGCTGCAGTGCTGGCGGCCGGGGGTGGGGGTGCAAGGACGGAGGCGGGGCGGGACC
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GCCGGCGACGTCACGACCGCCGGCCCCACCCCCACGTTCTCTGCCTCCGCCCCGCCCTGG 960
CCGGGCCACCACTCCTGCCACTCCGCAGCTCCAGCTCCCTGGAGAGGGGCATGCACATG
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GGCCCGGTGGTGGAGGACGGTGAGGCGTCGAGGTGAGGGACCTCTCCCCGTACGTGTAC 1020
CCCACGTCACCCACGTTTCTGGAGGGCAACACGGTGGTCTGA
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1062
GGGTGCAGTGGGTGCAAAGACCTCCCGTTGTGCCACCAGACT

FIGURE 16 A

1 MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
 51 NLLVLIIVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
 101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
 151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
 201 ILLAIVALLYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAP
 251 SILLLDYACP VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL
 301 RPLQCWRPGV GVQGRRRGGT PGHLLPLRS SSSLERGMHM PTSPTFLEGN
 351 TVV*

Conserved features of G-protein coupled receptors include:

N-terminal extracellular domain:	Residues 1 - 36
TM-I:	Residues 37 - 57
Intracellular loop 1:	Residues 58 - 68
TM-II:	Residues 69 - 92
Extracellular loop 1:	Residues 93 - 111
TM-III:	Residues 112 - 130
Intracellular loop 2:	Residues 131 - 149
TM-IV:	Residues 150 - 168
Extracellular loop 2:	Residues 169 - 185
TM-V:	Residues 186 - 210
Intracellular loop 3:	Residues 211 - 232
TM-VI:	Residues 233 - 254
Extracellular loop 3:	Residues 255 - 266
TM-VII:	Residues 267 - 285
C-terminal cytoplasmic domain:	Residues 286 - 353

Potential post-transcriptional modification sites:

N-glycosylation:	Residues 19
Phosphorylation:	Residues 142, 145, 219, 289, 332, 345
Myristylation:	Residues 141, 318

Figure 16B

Predicted amino acid sequence of HEDG4 polypeptide encoded by pC3-hedg4#36.

1 MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
51 NLLVLIAVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
201 ILLAVVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAF
251 SILLLDYACP VHSCPILYKA HYLFAVSTLN SLLNPVIYTW RSRDLRREVL
301 RPLQCWRPGV GVQGRRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN
351 TVV

Human	1	MGSLYSEYLNPKNKVQEHYN YTKETLETQETT SRQVASAFIVILCCAIVVE	50
Rat	1	MGGLYSEYLNPKEKVKQEHYN YTKETLDMQETPSRKVASAFII ILCCAIVVE	50
Human	51	NLLVLI A VARN SKFHSAM YLFLGNLA ASDLLAGVA FVAN TLLSGSVTLRL	100
Rat	51	NLLVLI A VARN SKFHSAM YLFLGNLA ASDLLAGVA FVAN TLLSGPVTLSL	100
Human	101	TPVQWFAREGS AFITLSAS VF SLLAIAIERHVA IAKVKLYGSDKSCRM LL	150
Rat	101	TPLQWFAREGS AFITLSAS VF SLLAIAIERQVA IAKVKLYGSDKSCRM LM	150
Human	151	LIGASWLISLV LGGLPILGW NCLGHLEACSTVL PLYAKHYVLCVV TI FSI	200
Rat	151	LIGASWLISLIL GGLPILGW NCLDHLEACSTVL PLYAKHYVLCVV TI FSV	200
Human	201	ILLAI VALYVR IYCVRSSHADMA APQTLALLKT VTIVLGVFIVCWLP AF	250
Rat	201	ILLAI VALYVR IYFVVRSSHADV AGPQTLALLKT VTIVLGVFII CWLP AF	250
Human	251	SILLLDYACP VHSCPILYKA HYXFAVSTLNSLL NPVIYTWRSRDLRRE VL	300
Rat	251	SILLLDSTCP VRACPVLYKA HYFFAFATLNSLL NPVIYTWRSRDLRRE VL	300
Human	301	RPLQCWRPGVG VQGRRRGGT PGHHLLPLRSSSS SLERGMHMPTSP TFLEG N	350
Rat	301	RPLL CWRQKGKATG . RRGNGNPGHR LLPLRSSSS SLERGLHMPTSP TFLEG N	349
Human	351	TVV* 353 	
Rat	350	TVV* 352	

Figure 17B

Alignment of HEDG4 with pC3-hedg4#36 translation product and rat H218 (REDG4). Differences between pC3-hedg4#36 translation product and previously determined HEDG4 polypeptide are indicated in reverse text. Differences between rat and human edg-4 polypeptide sequences are shown in bold, shaded text.

	1				50																																													
HEDG4	M	G	S	L	Y	S	E	Y	L	N	P	N	K	V	Q	E	H	Y	N	Y	T	K	E	T	L	E	T	Q	E	T	T	S	R	Q	V	A	S	A	F	I	V	I	L	C	C	A	I	V	V	E
HEDG4#36	M	G	S	L	Y	S	E	Y	L	N	P	N	K	V	Q	E	H	Y	N	Y	T	K	E	T	L	E	T	Q	E	T	T	S	R	Q	V	A	S	A	F	I	V	I	L	C	C	A	I	V	V	E
REDG4	M	G	S	L	Y	S	E	Y	L	N	P	N	K	V	Q	E	H	Y	N	Y	T	K	E	T	L	D	M	Q	E	T	T	S	R	Q	V	A	S	A	F	I	V	I	L	C	C	A	I	V	V	E
	51									100																																								
HEDG4	N	L	L	V	L	I	A	V	A	R	N	S	K	F	H	S	A	M	Y	L	F	L	G	N	L	A	A	S	D	L	L	A	G	V	A	F	V	A	N	T	L	L	S	G	S	V	T	L	R	L
HEDG4#36	N	L	L	V	L	I	A	V	A	R	N	S	K	F	H	S	A	M	Y	L	F	L	G	N	L	A	A	S	D	L	L	A	G	V	A	F	V	A	N	T	L	L	S	G	S	V	T	L	R	L
REDG4	N	L	L	V	L	I	A	V	A	R	N	S	K	F	H	S	A	M	Y	L	F	L	G	N	L	A	A	S	D	L	L	A	G	V	A	F	V	A	N	T	L	L	S	G	S	V	T	L	R	L
	101									150																																								
HEDG4	T	P	V	Q	W	F	A	R	E	G	S	A	F	I	T	L	S	A	S	V	F	S	L	L	A	I	A	I	E	R	H	V	A	I	A	K	V	K	L	Y	G	S	D	K	S	C	R	M	L	L
HEDG4#36	T	P	V	Q	W	F	A	R	E	G	S	A	F	I	T	L	S	A	S	V	F	S	L	L	A	I	A	I	E	R	H	V	A	I	A	K	V	K	L	Y	G	S	D	K	S	C	R	M	L	L
REDG4	T	P	V	Q	W	F	A	R	E	G	S	A	F	I	T	L	S	A	S	V	F	S	L	L	A	I	A	I	E	R	Q	V	A	I	A	K	V	K	L	Y	G	S	D	K	S	C	R	M	L	M
	151									200																																								
HEDG4	L	I	G	A	S	W	L	I	S	L	V	L	G	G	L	P	I	L	G	W	N	C	L	G	H	L	E	A	C	S	T	V	L	P	L	Y	A	K	H	Y	V	L	C	V	V	T	I	F	S	I
HEDG4#36	L	I	G	A	S	W	L	I	S	L	V	L	G	G	L	P	I	L	G	W	N	C	L	G	H	L	E	A	C	S	T	V	L	P	L	Y	A	K	H	Y	V	L	C	V	V	T	I	F	S	I
REDG4	L	I	G	A	S	W	L	I	S	L	V	L	G	G	L	P	I	L	G	W	N	C	L	D	H	L	E	A	C	S	T	V	L	P	L	Y	A	K	H	Y	V	L	C	V	V	T	I	F	S	I
	201									250																																								
HEDG4	I	L	L	A	V	V	A	L	Y	V	R	I	Y	C	V	V	R	S	S	H	A	D	M	A	A	P	Q	T	L	A	L	L	K	T	V	T	I	V	L	G	V	F	I	V	C	W	L	P	A	F
HEDG4#36	I	L	L	A	V	V	A	L	Y	V	R	I	Y	C	V	V	R	S	S	H	A	D	M	A	A	P	Q	T	L	A	L	L	K	T	V	T	I	V	L	G	V	F	I	V	C	W	L	P	A	F
REDG4	I	L	L	A	I	V	A	L	Y	V	R	I	Y	F	V	V	R	S	S	H	A	D	V	A	G	P	Q	T	L	A	L	L	K	T	V	T	I	V	L	G	V	F	I	I	C	W	L	P	A	F
	251									300																																								
HEDG4	S	I	L	L	L	D	Y	A	C	P	V	H	S	C	P	I	L	Y	K	A	H	Y	X	F	A	V	S	T	L	N	S	L	L	N	P	V	I	Y	T	W	R	S	R	D	L	R	R	E	V	L
HEDG4#36	S	I	L	L	L	D	Y	A	C	P	V	H	S	C	P	I	L	Y	K	A	H	Y	X	F	A	V	S	T	L	N	S	L	L	N	P	V	I	Y	T	W	R	S	R	D	L	R	R	E	V	L
REDG4	S	I	L	L	L	D	S	T	C	P	V	R	A	C	P	V	L	Y	K	A	H	Y	E	F	A	F	A	T	L	N	S	L	L	N	P	V	I	Y	T	W	R	S	R	D	L	R	R	E	V	L
	301									350																																								
HEDG4	R	P	L	Q	C	W	R	P	G	V	G	V	Q	G	R	R	R	G	G	T	P	G	H	H	L	L	P	L	R	S	S	S	S	L	E	R	G	M	H	M	P	T	S	P	T	F	L	E	G	N
HEDG4#36	R	P	L	Q	C	W	R	P	G	V	G	V	Q	G	R	R	R	G	G	T	P	G	H	H	L	L	P	L	R	S	S	S	S	L	E	R	G	M	H	M	P	T	S	P	T	F	L	E	G	N
REDG4	R	P	L	Q	C	W	R	Q	G	K	G	A	T	G	.	R	R	G	G	N	P	G	H	R	L	L	P	L	R	S	S	S	S	L	E	R	G	L	H	M	P	T	S	P	T	F	L	E	G	N
	351																																																	
HEDG4	T	V	V	-																																														
HEDG4#36	T	V	V	-																																														
REDG4	T	V	V	-																																														

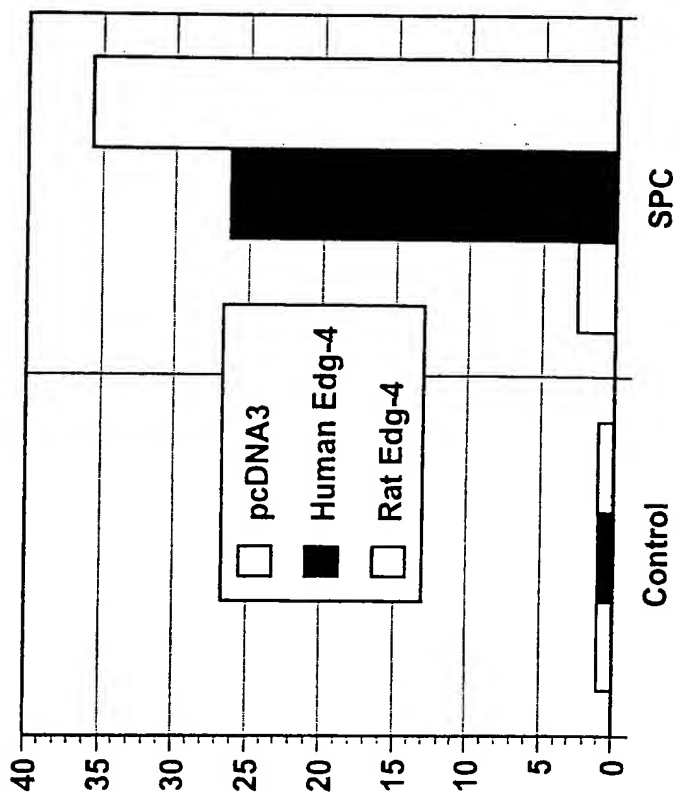


Figure 18A.

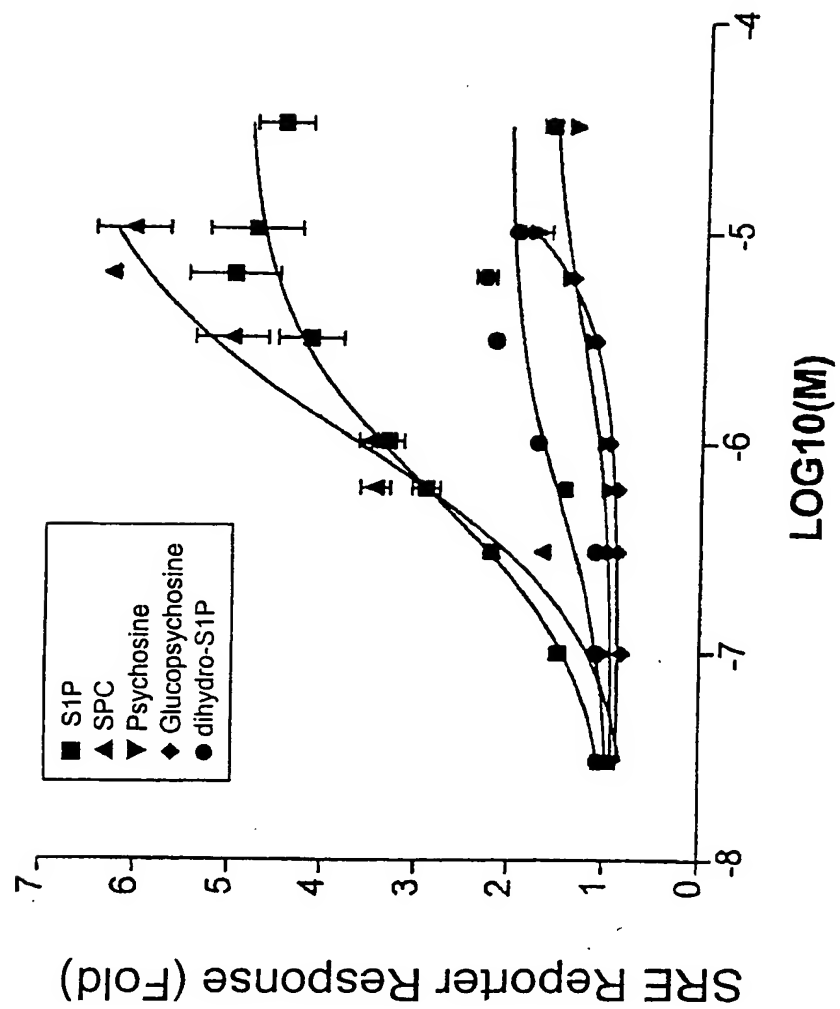
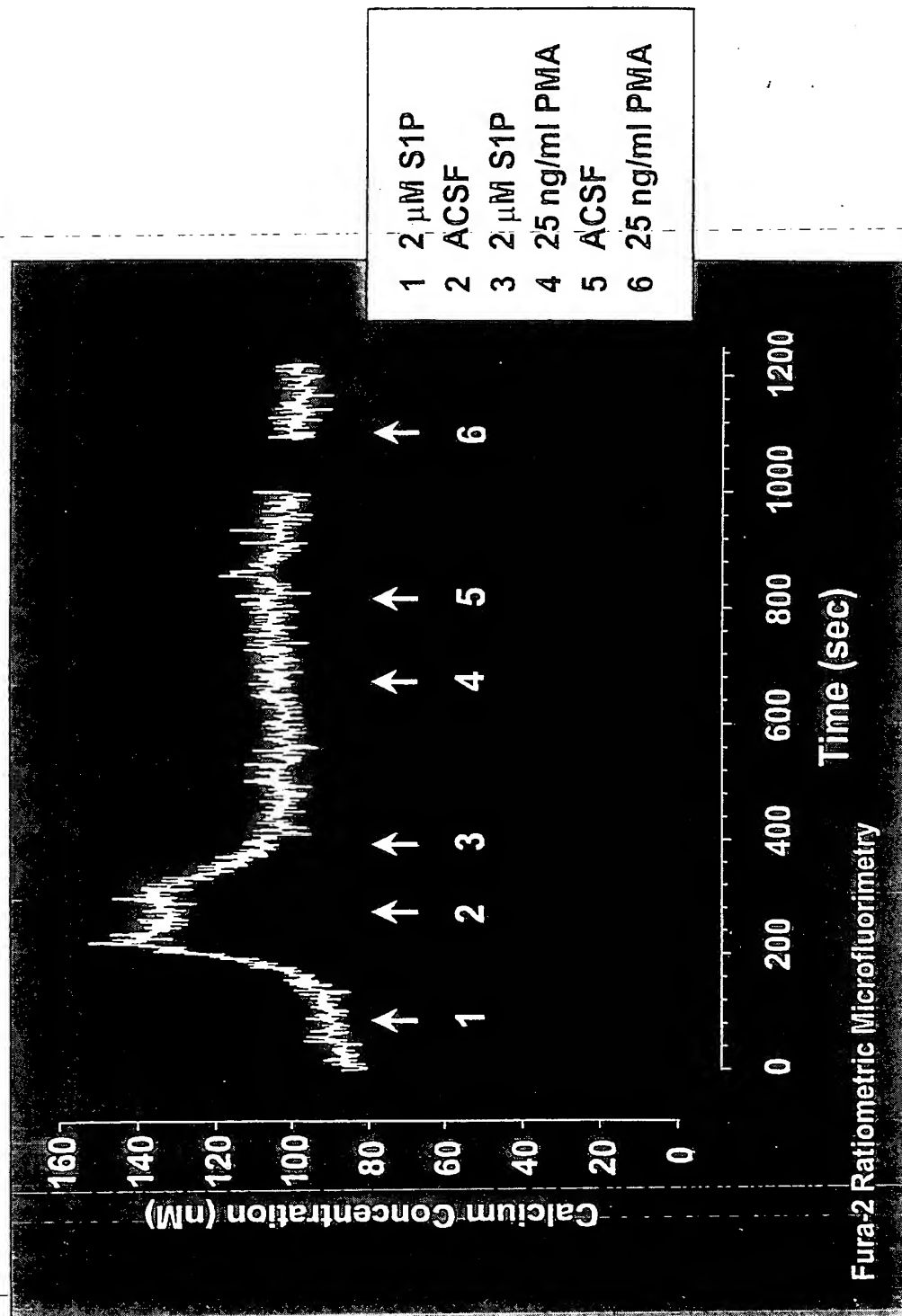


Figure 18B.

Figure 19.



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Figure 20.

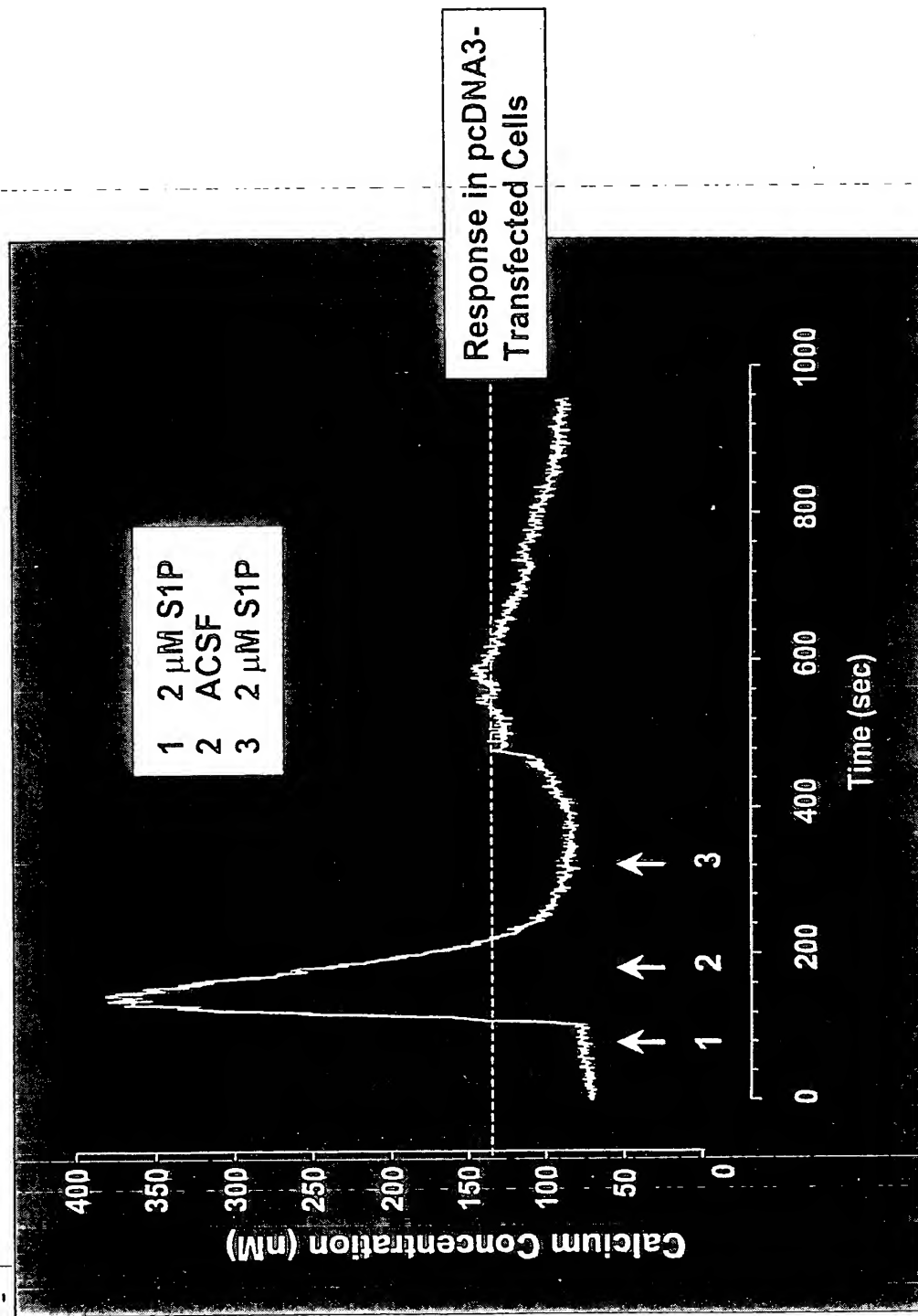


Figure 21. Human Edg-6 Amino Acid Sequence.

1 MVIMGQCYNETIGFFYNNSGKELSSHWRPKDVVVVALGLTVSVLVLLTNLLVIAAIASN 60
-----+-----+-----+-----+-----+-----+
61 RRFHQPIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDTSLTASVA 120
-----+-----+-----+-----+-----+-----+
121 TLLAIAVERHRVMAVQLHSRLPRGRVVMLIVGVVVAALGLGLLPAHSWHCLCALDRCSR 180
-----+-----+-----+-----+-----+-----+
181 MAPLLRSYLAVWALSSLLVFLLMVAVYTRIFFYVRRRVQRM AEHVSCHPRYRETTLSLV 240
-----+-----+-----+-----+-----+-----+
241 KTVVIILGAFVVCWTPGQVVLLLDGLGCESC NVLAVEKYFLLLAEANSLVNAAVYSCRDA 300
-----+-----+-----+-----+-----+-----+
301 EMRRTFRRLCCACL RQSTRESVHYTSSAQGGASTRIMLPENGHPLMDSTL* 352
-----+-----+-----+-----+-----+-----+

Figure 22. Human Edg-6 Sequence

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1   ATGGTCATCATGGGCCAGTGCTACTACAACGAGACCATCGGCTTCTTCTATAACAACAGT
   -----+-----+-----+-----+-----+-----+-----+
61  TACCAGTAGTACCCGGTCACGATGATGTTGCTCTGGTAGCCGAAGAAGATATTGTTGTCA
   -----+-----+-----+-----+-----+-----+-----+
   GGCAAAGAGCTCAGCTCCCACTGGCGGCCCAAGGATGTGGTCGTGGTGGCACTGGGGCTG
121 -----+-----+-----+-----+-----+-----+-----+
   CCGTTTCTCGAGTCGAGGGTGACCGCCGGGTTCTTACACCAGCACCACCGTGACCCCGAC
   -----+-----+-----+-----+-----+-----+-----+
181 ACCGTCAGCGTGCTGGTGCTGCTGACCAATCTGCTGGTCATAGCAGCCATCGCCTCCAAC
   -----+-----+-----+-----+-----+-----+-----+
   TGGCAGTCGCACGACCACGACGACTGGTTAGACGACCAGTATCGTCGGTAGCGGAGGTTG
   -----+-----+-----+-----+-----+-----+-----+
241 CGCCGCTTCCACCAGCCCATCTACTACCTGCTCGGCAATCTGGCCGCGGCTGACCTCTTC
   -----+-----+-----+-----+-----+-----+-----+
   GCGGCGAAGGTGGTCGGGTAGATGATGGACGAGCCGTTAGACCGGCGCCGACTGGAGAAG
   -----+-----+-----+-----+-----+-----+-----+
301 GCGGGCGTGGCCTACCTCTTCCTCATGTTCCACACTGGTCCCCGCACAGCCCGACTTTCA
   -----+-----+-----+-----+-----+-----+-----+
   CGCCCGCACCCGATGGAGAAGGAGTACAAGGTGTGACCAGGGGCGTGTGCGGGCTGAAAGT
   -----+-----+-----+-----+-----+-----+-----+
361 CTTGAGGGCTGGTTCCTGCGGCAGGGCTTGCTGGACACAAGCCTCACTGCGTCGGTGGCC
   -----+-----+-----+-----+-----+-----+-----+
   GAACTCCCCGACCAAGGACGCCGTCCCGAACGACCTGTGTTGCGAGTGACGCAGCCACCGG
   -----+-----+-----+-----+-----+-----+-----+
421 ACACTGCTGGCCATCGCCGTGGAGCGGCACCGCAGTGTGATGGCCGTGCAGCTGCACAGC
   -----+-----+-----+-----+-----+-----+-----+
   TGTGACGACCGGTAGCGGCACCTCGCCGTGGCGTCACACTACCGGCACGTGCAGCTGTGC
   -----+-----+-----+-----+-----+-----+-----+
481 CGCCTGCCCCGTGGCCGCGTGGTCATGCTCATTGTGGGCGTGTGGGTGGCTGCCCTGGGC
   -----+-----+-----+-----+-----+-----+-----+
   GCGGACGGGGCACCGGCGCACCACTACGAGTAACACCCGCACACCCACCGACGGGACCCG
   -----+-----+-----+-----+-----+-----+-----+
541 CTGGGGCTGCTGCCTGCCCCTCCTGGCACTGCCTCTGTGCCCTGGACCGCTGCTCACGC
   -----+-----+-----+-----+-----+-----+-----+
   GACCCCGACGACGGACGGGTGAGGACCGTGACGGAGACACGGGACCTGGCGACGAGTGCG
   -----+-----+-----+-----+-----+-----+-----+
601 ATGGCACCCTGCTCAGCCGCTCCTATTGGCCGTCTGGGCTCTGTGAGCCTGCTTGTC
   -----+-----+-----+-----+-----+-----+-----+
   TACCGTGGGGACGAGTCGGCGAGGATAAACCCGCAGACCCGAGACAGCTCGGACGAACAG
   -----+-----+-----+-----+-----+-----+-----+
661 TTCCTGCTCATGGTGGCTGTGTACACCCGCATTTTCTTCTACGTGCGGCGGCGAGTGCAG
   -----+-----+-----+-----+-----+-----+-----+
   AAGGACGAGTACCACCGACACATGTGGGCGTAAAAGAAGATGCACGCCGCCGCTCACGTC
   -----+-----+-----+-----+-----+-----+-----+
721 CGCATGGCAGAGCATGTCAGCTGCCACCCCGCTACCGAGAGACCACGCTCAGCCTGGTC
   -----+-----+-----+-----+-----+-----+-----+
   GCGTACCGTCTCGTACAGTCGACGGTGGGGCGATGGCTCTCTGGTGCAGTTCGGACCAG
   -----+-----+-----+-----+-----+-----+-----+
781 AAGACTGTTGTCATCATCCTGGGGGCGTTCTGGTCTGCTGGACACCAGGCCAGGTGGTA
   -----+-----+-----+-----+-----+-----+-----+
   TTCTGACAACAGTAGTAGGACCCCCGCAAGCACCAGACGACCTGTGGTCCGGTCCACCAT
   -----+-----+-----+-----+-----+-----+-----+
840 CTGCTCCTGGATGGTTTAGGCTGTGAGTCCTGCAATGTCTGGCTGTAGAAAAGTACTTC
   -----+-----+-----+-----+-----+-----+-----+
   GACGAGGACCTACCAAATCCGACACTCAGGACGTTACAGGACCGACATCTTTTCATGAAG

```


841 CTACTGcTGGCCGAGGCCAACTCACTGGTCAATGCTGCTGTGTACTCTTGCCGAGATGCT
-----+-----+-----+-----+-----+-----+-----+
GATGACgACCGGCTCCGGTTGAGTGACCAGTTACGACGACACATGAGAACGGCTCTACGA 900

901 GAGATGCGCCGCACCTTCCGCCGCCCTTCTCTGCTGCGCGTGCCTCCGCCAGTCCACCCGC
-----+-----+-----+-----+-----+-----+-----+
CTCTACGCGGCGTGGAAGGCGGCGGAAGAGACGACGCGCACGGAGGCGGTGAGGTGGGCG 960

961 GAGTCTGTCCACTATACATCCTCTGCCCAGGGAGGTGCCAGCACTCGCATCATGCTTCCC
-----+-----+-----+-----+-----+-----+-----+
CTCAGACAGGTGATATGTAGGAGACGGGTCCCTCCACGGTCGTGAGCGTAGTACGAAGGG 1020

1021 GAGAACGGCCACCCACTGATGGACTCCACCCTTTAG
-----+-----+-----+-----+-----+-----+-----+
CTCTTGCCGGTGGGTGACTACCTGAGGTGGGAAATC 1056

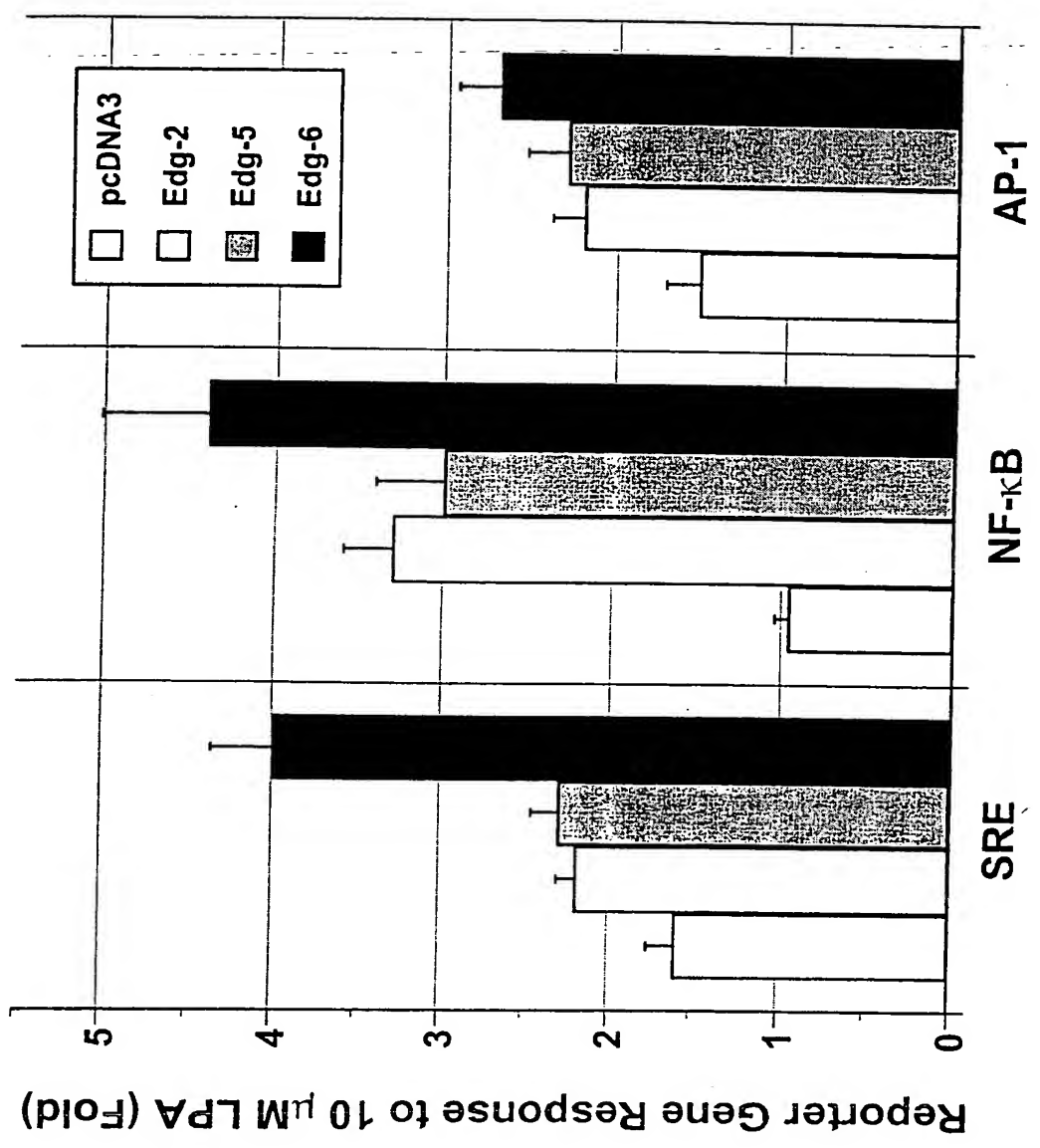


Figure 23.

Figure 24.

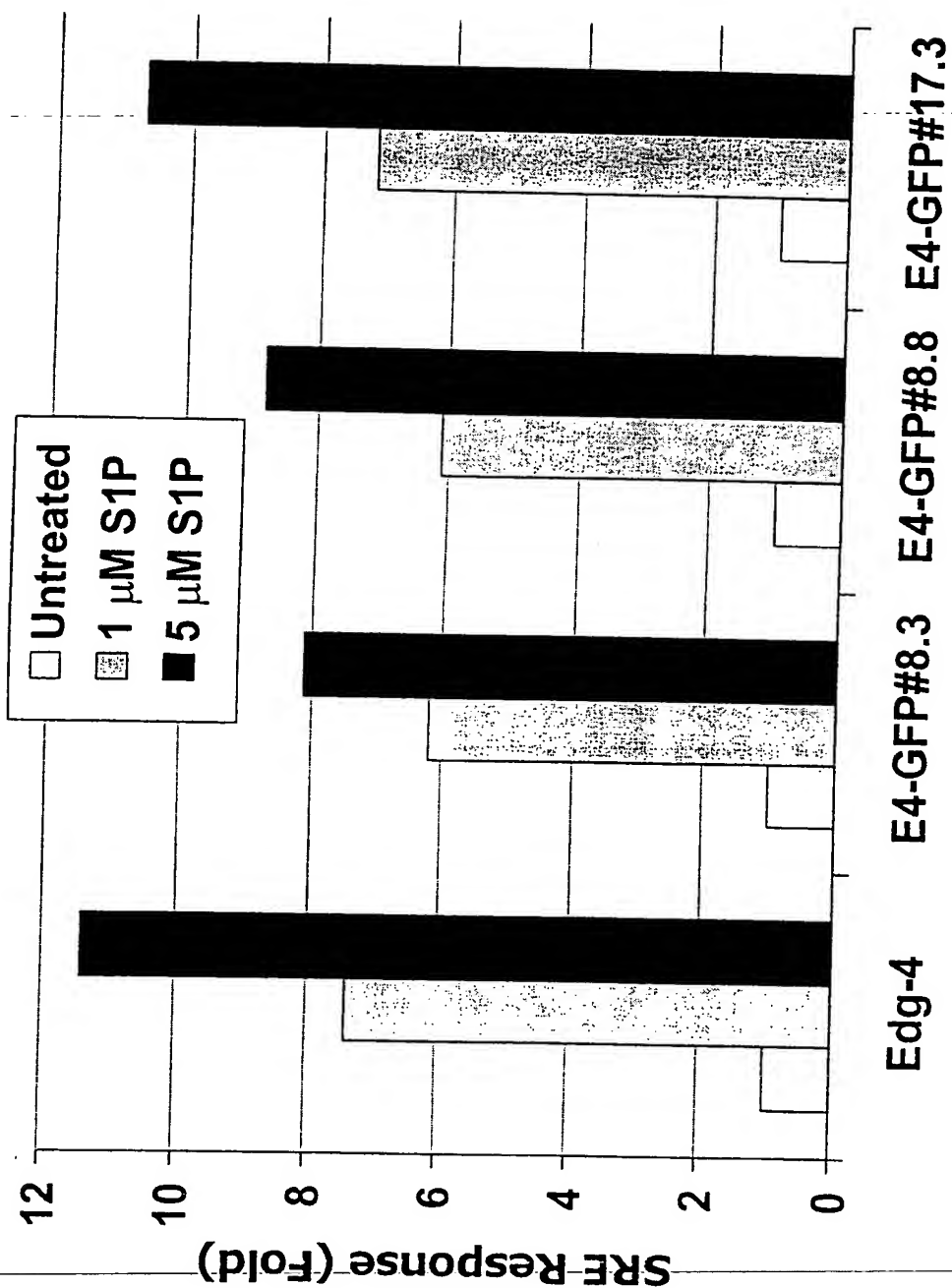


Figure 25.

